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RAW SEQUENCE LISTING DATE: 12/10/2001 PATENT APPLICATION: US/09/902,460 TIME: 11:25:51
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Input Set : N:\Crf3\RULE60\09902460.txt
Output Set: N:\CRF3\12102001\I902460.raw

SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
             (i) APPLICANT: FIDDES, J.C.
      5
                             ABRAHAM, J.D.
      6
            (ii) TITLE OF INVENTION: HUMAN BASIC FIBROBLAST GROWTH
      8
                                      FACTOR ANALOG
      9
           (iii) NUMBER OF SEQUENCES: 69
     11
            (iv) CORRESPONDENCE ADDRESS:
     13
                   (A) ADDRESSEE: MORRISON & FOERSTER
     14
                   (B) STREET: 755 PAGE MILL ROAD
     15
                   (C) CITY: Palo Alto
     16
                                                           ENTERED
     17
                   (D) STATE: CA
                   (E) COUNTRY: USA
     18
                  (F) ZIP: 94304-1018
     19
             (V) COMPUTER READABLE FORM:
     21
                   (A) MEDIUM TYPE: Diskette
     22
                   (B) COMPUTER: IBM Compatible
     23
                   (C) OPERATING SYSTEM: Windows
     24
                   (D) SOFTWARE: FastSEQ for Windows Version 2.0b
     25
            (vi) CURRENT APPLICATION DATA:
     27
                   (A) APPLICATION NUMBER: US/09/902,460
C--> 28
                   (B) FILING DATE: 09-Jul-2001
C--> 29
                   (C) CLASSIFICATION:
     30
           (vii) PRIOR APPLICATION DATA:
     32
                   (A) APPLICATION NUMBER: 09/098,628
     33
                   (B) FILING DATE: 1998-06-16
     34
          (viii) ATTORNEY/AGENT INFORMATION:
     38
     39
                   (A) NAME: Lehnhardt, Susan K
                   (B) REGISTRATION NUMBER: 33,943
     40
                   (C) REFERENCE/DOCKET NUMBER: 21900-20089.10
     41
            (ix) TELECOMMUNICATION INFORMATION:
     43
     44
                   (A) TELEPHONE: 650-813-5600
                   (B) TELEFAX: 650-494-0792
     45
                   (C) TELEX: 706141
     46
     49 (2) INFORMATION FOR SEQ ID NO: 1:
             (i) SEQUENCE CHARACTERISTICS:
     51
                   (A) LENGTH: 1969 base pairs
     52
                   (B) TYPE: nucleic acid
     53
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                   (C) STRANDEDNESS: double
                   (D) TOPOLOGY: linear
     55
            (ii) MOLECULE TYPE: cDNA
     57
            (ix) FEATURE:
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                   (A) NAME/KEY: Coding Sequence
     60
     61
                   (B) LOCATION: 970...1434
                   (D) OTHER INFORMATION:
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            (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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Input Set : N:\Crf3\RULE60\09902460.txt
Output Set: N:\CRF3\12102001\I902460.raw

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100 100	67		
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GTTTGGTGG TGCGGGGGTT GGCCGGGGGT GACTTTTGGG GGATAAGGGC CGGTGGAGCC CAGGGAGTC CAGGGAGTC CAGGGAGTC CCAGGCCCCC CCCCGCCCC TGGCCTTCCC	69		
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CCGCCCCCG ACTGAGGCCG GGCTCCCGC CGGACTGATG TCGCGGCGTT GCGTGTTGTC 480 GCGAAGCCG CCGAAACTCAG AGGCCGGCCC CAGAAAACCC GAGCGATGAG GGGCGGGCCC	71	GTTTGGGTGG TGCGGGGGTT GGGCGGGGGT GACTTTTGGG GGATAAGGGG CGGTGGAGCC	360
GCGAAGGCCG CCGAACTCAG AGGCCGCCC CAGAAAACCCC GAGGAGTAG GGGCGGCGCC 540	72	CAGGGAATGC CAAAGCCCTG CCGCGGCCTC CGACGCGCGC CCCCCGCCCC TCGCCTCTCC	420
GCGAAGGCCG CCGAACTCAG AGGCCGCCC CAGAAAACCCC GAGGAGTAG GGGCGGCGCC 540	73		480
GCAGGAGGA GAGAACTGG GGGCGCGGA GCTGGTGGG TGTGGGGGGGT GCAGATGTAG			540
66 AGARTAGGAC GCCGCGGCCC GGCGGTGCCA AGCGGTGCCCC GGGGTTGCAA 660 77 CGGGATCCCG GGCGCTGCAG CTTGGGAGGC GGCTCTCCCC AGGCGGCGTC CGCGGAGACA 720 78 CCCATCTGTC AACCCCAGGT CTGGGAGGC GCGCTCGCCG AGGCGGCGCCG 780 79 AGAAGACGG AACCCAGGT CCCGGGCCGC CGCGCCGCGC			600
CCCATCTCTG GACCCTGCAG CTTGGGAGGG GGCTCTCCCC AGGCGGCGTC CGCGAGACA 780			660
CCCATCTGTC AACCCCAGGT CCCGGGCCGC CGGCTGGCGG GCCAGGGG GCCGGGGAC AGAAGAGCGG CCCAGGGGT CGAGGCTGG GGACCGCGGG GCCGGCGGGCCGG 840 CCGAGGGCTG GGGGCCGGG CCCGGGGCCC GCCCGCGGGCCCC 960 GGCCGGGGA CGGCGGCTC CCGCGGGCT CCAGCGGCTC GGGGATCCCG GCCGGGCCCC 960 GGCCGGGGA CGGCGGCTC CCGCGGGGCT CCAGCGGCTC GGGGATCCCG GCCGGGCCCC 960 GGCCGGGGACC ATG GCA GCC GGC ACC ATC ACC ACG CTG CCC GCC TTG CCC GAC 1011 Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu			720
AGARGAGGG CCGAGCGGGC CGAGGCTGGG GGAGCCGGG CGCGGCCGG CGCGGGCCGG CGGGGCCGG CGGGGGCGG GGGGGG			780
CGGGAGGCTG GGGGGCCGGG GCCGGGGGCCG TGCCCGGAGG GGGTCGGAGG CCGGGCCCC GGGGGCCCC GGGGGCAC CGGCGGGAC CCGGCGGCCCC CGGGGGCCC CAGGGGCCC GGGGACCATG GCA GGCAC AGG ACA ATC ACC ACG CTG CCC GCC TTG CCC GAC 1011 Sa			
81 GGCCGGGGGA CGGCGGCTC CCGCGCGGGCT CCAGCGGCTC GGGGATCCCG GCCGGGCCCC GCCGGGCCCC GCCGGGCCCC GCCGGGCCCC GCCGGGCCCC GCCGGGAGCCCC GCCAGGAGCACC ATG GCA GCC GGG AGC ATC ACC ACG CTG CCC GCC TTG CCC GAG 1011			
Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu			
Met Ala Ala Gly Ser Ile Thr Thr Leu Pro Ala Leu Pro Glu			
84			1011
### REPRESENTATION OF COMMENT OF			
87 Asp Gly Gly Ser Gly Ala Phe Pro Pro Gly His Phe Lys Asp Pro Lys 88 15 20 25 30 90 CGG CTG TAC TGC AAA AAC GGG GGC TTC TTC CTG CGC ATC CAC CCC GAC 1107 91 Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp 92 35 40 45 94 GGC CGA GTT GAC GGG GTC CGG GAG AAG AGC GAC CCT CAC ATC AAG CTA 1155 95 GJy Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu 96 50 55 60 98 CAA CTT CAA GCA GAA GAG AGA GGA GTT GTG TCT ATC AAA GGA GTG TGT 1203 99 Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys 100 65 70 75 102 GCT AAC CGT TAC CTG GCT ATG AAG GAA GAA GAA GAT GGA AGA ATA CTG GCT TCT 1251 103 Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser 104 80 85 90 106 AAA TGT GTT ACG GAT GAG TGT TTC TTT TTT GAA CGA TTG GAA TCT AAT 1299 107 Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn 108 95 100 105 110 110 AAC TAC AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA 1347 111 Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala 112 115 120 125 114 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 115 Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly 116 130 135 140 117 CAG AAA GCT ATA CTT TTT CTA TCT GCT AGA ACC TGT TTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 120 145 150 155 122 CCACATCTAA TCTCATTTCA CAGGTATAA AGAGATATT TATAATAATTT GTTAATGAGA 1506 124 AGTAGTAAAA TATGTACACC ATGCCCAGTAA AGAAAATAA CAAAAAGTTGT AAAAATTTATAA 1626		<u> </u>	1050
15			1039
90 CGG CTG TAC TGC AAA AAC GGG GGC TTC TTC CTG CGC ATC CAC CCC GAC 1107 91 Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp 35 40 45 94 GGC CGA GTT GAC GGG GTC CGG GAG AAG AGC GAC CCT CAC ATC AAG CTA 1155 95 Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu 50 55 60 98 CAA CTT CAA GCA GAA GAG AGA GGA GTT GTG TCT ATC AAA GGA GTG TGT 1203 99 Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys 100 65 70 75 102 GCT AAC CGT TAC CTG GCT ATG AAG GAA GAA AGA AGA AGA TTA CTG GCT TCT 1251 103 Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser 104 80 85 90 106 AAA TGT GTT ACG GAT GAG TGT TCT TTT TTT GAA CGA TTG GAA TCT AAT 1299 107 Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn 108 95 100 105 110 110 AAC TAC AAT ACT TAC CGG TCA AGG AAA TAC ACC ACT TGG TAT GTG GCA 1347 111 Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala 112 125 120 125 114 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 115 Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly 116 130 135 140 118 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 120 145 150 155 122 CCACATCTAA TCTCATTCA CATGAAAGAA GAAGAAATAT GAAAAGTTG TAAAATTT CTTAATACAA TTTTTTATCC 1566 124 AGTAGAAAAA TAAAAAAATAAA TAAGCTCAGT TTGGATAATT TTAAGAAATTT GTTAATGAGA 1506			
91 Arg Leu Tyr Cys Lys Asn Gly Gly Phe Phe Leu Arg Ile His Pro Asp 92 35 40 45 94 GGC CGA GTT GAC GGG GTC CGG GAG AAG AGC GAC CCT CAC ATC AAG CTA 1155 95 Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu 96 50 55 60 98 CAA CTT CAA GCA GAA GAG AGA GGA GTT GTG TCT ATC AAA GGA GTG TGT 1203 99 Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys 100 65 70 75 102 GCT AAC CGT TAC CTG GCT ATG AAG GAA GAT GGA AGA TTA CTG GCT TCT 1251 103 Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser 104 80 85 90 106 AAA TGT GTT ACG GAT GAG TGT TTC TTT TTT GAA CGA TTG GAA TCT AAT 1299 107 Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn 108 95 100 105 110 10 AAC TAC AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA 1347 111 Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala 112 115 120 125 114 TTG AAA CGA ACT GGG CAG TA AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 115 Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly 116 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GAT AAG AGC TGATTTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 120 145 150 155 122 CCACATCTAA TCTCATTCA CATGAAAGAA GAAGATATAT TTAGAAAATTT GTTAATGAGA 1506 123 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT TTAGAAATTT GTTAATGAGA 1506 124 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626		15	1107
92			1107
94 GGC CGA GTT GAC GGG GTC CGG GAG AAG AGC GAC CCT CAC ATC AAG CTA 1155 95 Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu 96 50 55 60 98 CAA CTT CAA GCA GAA GAG AGA GAG GGA GTT GTG TCT ATC AAA GGA GTG TGT 1203 99 Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys 100 65 70 75 102 GCT AAC CGT TAC CTG GCT ATG AAG GAA GAT GGA AGA TTA CTG GCT TCT 1251 103 Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser 104 80 85 90 106 AAA TGT GTT ACG GAT GAT TGT TTC TTT TTT GAA CGA TTG GAA TCT AAT 1299 107 Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn 108 95 100 105 110 110 AAC TAC AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA 1347 111 Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala 112 125 125 114 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 115 Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly 130 135 140 118 CAG AAA GCT ATA CTT TCT CCA ATG TCT GCT AAG AGC TGATTTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 120 145 150 155 122 CCACATCTAA TCTCATTCA CATGAAAGAA GAAGATATT TTAGAAATTT GTTAATGAGA 1506 123 GTAAAAGAAA ATAAATGTGT ATAGCCCAGTT TTGGATAATTA CAAAAGTTGT AAAATGTATA 1626	91		
95 Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu 96 50 55 60 98 CAA CTT CAA GCA GAA GAG AGA GAG AGA GGA GTT GTG TCT ATC AAA GGA GTG TGT 1203 99 Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys 100 65 70 75 102 GCT AAC CGT TAC CTG GCT ATG AAG GAA GAT GGA AGA TTA CTG GCT TCT 1251 103 Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser 104 80 85 90 106 AAA TGT GTT ACG GAT GAG TGT TTC TTT TTT GAA CGA TTG GAA TCT AAT 1299 107 Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn 108 95 100 105 110 110 AAC TAC AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA 1347 111 Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala 112 115 120 125 114 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 115 Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly 116 130 135 140 118 CAG AAA GCT ATA CTT TC CCA ATG TCT GCT AAG AGC TGATTTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 120 145 150 122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGATATAT TTAGAAAATTT GTTAATGAGA 1506 123 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATTA CAAAAGTTGT AAAATGTATA 1626	92		
96	94		1155
98 CAA CTT CAA GCA GAA GAG AGA GAG AGA GGA GTT GTG TCT ATC AAA GGA GTG TGT 99 Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys 100 65 70 75 102 GCT AAC CGT TAC CTG GCT ATG AAG GAA GAT GGA AGA TTA CTG GCT TCT 103 Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser 104 80 85 90 106 AAA TGT GTT ACG GAT GAG TGT TTC TTT TTT GAA CGA TTG GAA TCT AAT 1299 107 Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn 108 95 100 105 110 110 AAC TAC AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA 1347 111 Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala 112 115 120 125 114 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 115 Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly 116 130 135 140 118 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 120 145 150 155 122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA 1506 123 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC 1566 124 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626	95	Gly Arg Val Asp Gly Val Arg Glu Lys Ser Asp Pro His Ile Lys Leu	
99 Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys 100 65 70 75 102 GCT AAC CGT TAC CTG GCT ATG AAG GAA GAT GGA AGA TTA CTG GCT TCT 1251 103 Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser 104 80 85 90 106 AAA TGT GTT ACG GAT GAG TGT TTC TTT TTT GAA CGA TTG GAA TCT AAT 1299 107 Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn 108 95 100 105 110 110 AAC TAC AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA 1347 111 Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala 112 115 120 125 114 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 115 Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly 116 130 135 140 118 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 120 145 150 155 122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA 1506 123 GTAAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC 1566 124 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626	96	50 55 60	
100	98		1203
102 GCT AAC CGT TAC CTG GCT ATG AAG GAA GAT GGA AGA TTA CTG GCT TCT 103 Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser 104 80 85 90 106 AAA TGT GTT ACG GAT GAG TGT TTC TTT TTT GAA CGA TTG GAA TCT AAT 1299 107 Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn 108 95 100 105 110 110 AAC TAC AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA 1347 111 Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala 112 115 120 125 114 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 115 Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly 116 130 135 140 118 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 120 145 150 155 122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAAATTT GTTAATGAGA 1506 123 GTAAAAGAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626	99	Gln Leu Gln Ala Glu Glu Arg Gly Val Val Ser Ile Lys Gly Val Cys	
103 Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser 104 80 85 90 106 AAA TGT GTT ACG GAT GAG TGT TTC TTT TTT GAA CGA TTG GAA TCT AAT 1299 107 Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn 108 95 100 105 110 110 AAC TAC AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA 1347 111 Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala 112 115 120 125 114 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 115 Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly 116 130 135 140 118 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 120 145 150 155 122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA 1506 123 GTAAAAGAAA TAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC 1566 124 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAATAA CAAAAGTTGT AAAATGTATA 1626	100	65 70 75	
104 80 85 90 106 AAA TGT GTT ACG GAT GAG TGT TTC TTT TTT GAA CGA TTG GAA TCT AAT 1299 107 Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn 108 108 95 100 105 110 110 AAC TAC AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA 1347 111 Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala 112 125 114 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 115 120 125 116 130 135 140 118 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 120 155 120 140 155 156 122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA TTTTTAATC GTTAATGAGA 1506 123 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC TTTTTTTTTT	102	GCT AAC CGT TAC CTG GCT ATG AAG GAA GAT GGA AGA TTA CTG GCT TCT	1251
106 AAA TGT GTT ACG GAT GAG TGT TTC TTT TTT GAA CGA TTG GAA TCT AAT 1299 107 Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Glu Arg Leu Glu Ser Asn 100 105 110 110 AAC TAC AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA 1347 111 Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala 112 125 114 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 115 120 125 114 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 115 130 135 140 118 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 155 122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA 1506 123 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC 1566 124 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626	103	Ala Asn Arg Tyr Leu Ala Met Lys Glu Asp Gly Arg Leu Leu Ala Ser	
107 Lys Cys Val Thr Asp Glu Cys Phe Phe Phe Phe Glu Arg Leu Glu Ser Asn 108 95 100 105 110 110 110 105 110 111 AAC TAC AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA 1347 111 Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala 112 112 115 120 125 114 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 115 Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly 130 135 140 118 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG 1446 146 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 155 122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA 1506 123 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC 1566 124 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAAATAA CAAAAGTTGT AAAATGTATA 1626	104		
108 95 100 105 110 110 AAC TAC AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA 1347 111 ASN TYF ASN THE TYF AFG SEF AFG LYS TYF THE SEF TFF TYF VAL ALA 120 125 114 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 115 Leu Lys Arg The Gly Gln Tyr Lys Leu Gly Ser Lys The Gly Pro Gly 130 135 140 118 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 120 155 120 145 150 155 122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA 1506 123 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC 1566 124 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626	106	AAA TGT GTT ACG GAT GAG TGT TTC TTT TTT GAA CGA TTG GAA TCT AAT	1299
108 95 100 105 110 110 AAC TAC AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA 1347 111 ASN TYF ASN THE TYF AFG SEF AFG LYS TYF THE SEF TFF TYF VAL ALA 120 125 114 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 115 Leu Lys Arg The Gly Gln Tyr Lys Leu Gly Ser Lys The Gly Pro Gly 130 135 140 118 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 120 155 120 145 150 155 122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA 1506 123 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC 1566 124 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626	107		
110 AAC TAC AAT ACT TAC CGG TCA AGG AAA TAC ACC AGT TGG TAT GTG GCA 111 Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala 112 120 125 114 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 115 Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly 116 130 135 140 118 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 120 145 150 155 122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA 1506 123 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC 1566 124 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626			
111 Asn Tyr Asn Thr Tyr Arg Ser Arg Lys Tyr Thr Ser Trp Tyr Val Ala 112 115 120 125 114 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 115 Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly 116 130 135 140 118 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 120 145 150 155 122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA 1506 123 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC 1566 124 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626			1347
112 115 120 125 114 TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 115 Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly 116 130 135 140 118 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 120 145 150 155 122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA 1506 123 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC 1566 124 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626			
TTG AAA CGA ACT GGG CAG TAT AAA CTT GGA TCC AAA ACA GGA CCT GGG 1395 Leu Lys Arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly 130 135 140 138 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 120 145 150 155 122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA 1506 123 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC 1566 124 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626			
Leu Lys arg Thr Gly Gln Tyr Lys Leu Gly Ser Lys Thr Gly Pro Gly 116 130 135 140 118 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 120 145 150 155 122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA 1506 123 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC 1566 124 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626			1395
116 130 135 140 118 CAG AAA GCT ATA CTT TTT CTT CCA ATG TCT GCT AAG AGC TGATTTTAAT GG 1446 119 Gln Lys Ala Ile Leu Phe Leu Pro Met Ser Ala Lys Ser 120 145 150 155 122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA 1506 123 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC 1566 124 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626			
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120 145 150 155 122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA 1506 123 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC 1566 124 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626			T440
122 CCACATCTAA TCTCATTTCA CATGAAAGAA GAAGTATATT TTAGAAATTT GTTAATGAGA 1506 123 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC 1566 124 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626		-	
123 GTAAAAGAAA ATAAATGTGT ATAGCTCAGT TTGGATAATT GGTCAAACAA TTTTTTATCC 1566 124 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626			1506
124 AGTAGTAAAA TATGTAACCA TGCCCAGTAA AGAAAAATAA CAAAAGTTGT AAAATGTATA 1626			
125 TTCTCCCTTT TATATTGCAT CTGCTGTTAC CCAGTGAAGC TTACCTAGAG CAATGATCTT 1686			
	125	TTCTCCCTTT TATATTGCAT CTGCTGTTAC CCAGTGAAGC TTACCTAGAG CAATGATCTT	T989

Input Set : N:\Crf3\RULE60\09902460.txt
Output Set: N:\CRF3\12102001\I902460.raw

126 127 128 129 130 132 134 135 136 137 138 140	ATTTCTTCAT GGAAATCATA TACATTAGAA AATCACAGTC AGATGTTTAA TCAATCCAAA AATGTCCACT ATTTCTTATG TCATTCGTTA GTCTACATGT TTCTAAACAT ATAAATGTGA ATTTAATCAA TTCCTTTCAT AGTTTTATAA TTCTCTGGCA GTTCCTTATG ATAGAGTTTA TAAAACAGTC CTGTGTAAAC TGCTGGAAGT TCTTCCGGAA TTC (2) INFORMATION FOR SEQ ID NO: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 155 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein												1746 1806 1866 1926 1969		
143	3 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:														
145															
146															
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149	· · · · · · · · · · · · · · · · · · ·														
150	35 40 45														
151	_														
152	55 60														
153	Gln Ala	Glu Gl	ı Arg	Gly	Val	Val	Ser	Ile	Lys	Gly	Val	Cys	Ala		
154	65 70 75 80														
155	Arg Tyr	Leu Al	a Met	Lys	Glu	Asp	Gly		Leu	Leu	Ala	Ser		Cys	
156			85					90					95	_	
157	Val Thr	_	_	Phe	Phe	Phe		Arg	Leu	Glu	Ser		Asn	Tyr	
158		10		_	_	_	105		_		**- 3	110	.	T	
159	Asn Thr	=	g Ser	Arg	Lys		Thr	ser	Trp	Tyr		Ala	ьeu	гàз	
160		115		T	T	120	a	T	m h	G1	125	C1	Cln	T ***	
161	Arg Thr	GIA GI	n Tyr	ьys		GTĀ	ser	гуѕ	1111	140	PIO	СТА	GIII	цуѕ	
162 163	130 Ala Ile	rou Dh	. T.O.I	Dro	135	Cor	λla	Tvc	Cor	140					
164	145	Leu Pii	= Leu	150	Met	SCI	AIG	пуз	155						
166	(2) INFO	рматт∩и	FOR		או חד) · 3			133						
168	· ,	SEQUEN													
169	(-)	(A) L													
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178		(B) L	CATI	ON:	91	. 555									
179		(D) O	THER	INFO	RMAT	ION:									
181		SEQUEN													
183	TGCATTT'														60
184 GAAAGCGCCA CAAGCAGCAG CTGCTGAGCC ATG GCT GAA GGG GAA ATC ACC ACC 114 185 Met Ala Glu Gly Glu Ile Thr Thr												114			
185							Me	et A	La G	Lu G	Ly G	Lu I	le Tl	hr Thr	

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Output Set: N:\CRF3\12102001\1902460.raw

186										l				5			
188	TTC	ACA	GCC	CTG	ACC	GAG	AAG	TTT	AAT	CTG	ССТ	CCA	GGG	AAT	TAC	AAG	162
189										Leu							
190		10					15					20	-		•	-	
192	AAG	CCC	AAA	CTC	CTC	TAC	TGT	AGC	AAC	GGG	GGC	CAC	TTC	CTG	AGG	ATC	210
193										Gly							
194	25		-			30	-			-	35				-	40	
196	CTT	CCG	GAT	GGC	ACA	GTG	GAT	GGG	ACA	AGG	GAC	AGG	AGC	GAC	CAG	CAC	258
197										Arg							
198			-	-	45		_	_		50	_			_	55		
200	ATT	CAG	CTG	CAG	CTC	AGT	GCG	GAA	AGC	GTG	GGG	GAG	GTG	TAT	ATA	AAG	306
201	Ile	Gln	Leu	Gln	Leu	Ser	Ala	Glu	Ser	Val	Gly	Glu	Val	Tyr	Ile	Lys	
202				60					65					70			
204	AGT	ACC	GAG	ACT	GGC	CAG	TAC	TTG	GCC	ATG	GAC	ACC	GAC	GGG	CTT	TTA	354
205	Ser	Thr	Glu	Thr	Gly	Gln	Tyr	Leu	Ala	Met	Asp	Thr	Asp	Gly	Leu	Leu	
206			75					80					85				
208	TAC	GGC	TCA	CAG	ACA	CCA	AAT	GAG	GAA	TGT	TTG	TTC	CTG	GAA	AGG	CTG	402
209	Tyr	Gly	Ser	Gln	Thr	Pro	Asn	Glu	Glu	Cys	Leu	Phe	Leu	Glu	Arg	Leu	
210		90					95					100					
212	GAG	GAG	AAC	CAT	TAC	AAC	ACC	TAT	ATA	TCC	AAG	AAG	CAT	GCA	GAG	AAG	450
213	Glu	Glu	Asn	His	Tyr	Asn	Thr	Tyr	Ile	Ser	Lys	Lys	His	Ala	Glu	Lys	
214	105					110					115					120	
216										GGG							498
217	Asn	Trp	Phe	Val	Gly	Leu	Lys	Lys	Asn	Gly	Ser	Cys	Lys	Arg	Gly	Pro	
218					125					130					135		
220										TTG							546
221	Arg	Thr	His	Tyr	Gly	Gln	Lys	Ala	Ile	Leu	Phe	Leu	Pro	Leu	Pro	Val	
222				140					145					150			
224	TCT	TCT	GAT	TAA	AGAG	ATC I	rgtt(CTGG	GT G	rtga(CCAC!	r ccz	AGAGA	AAGT	TTC	GAGGGG	604
225	Ser	Ser	_														
226			155														620
228								TTCC		GΑ							638
230	(2)																
232		(1)						STICS		_							
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245 246	ASII	Leu	PLO	20	с⊥y	ASII	тАт	тλг	ьуs 25	FIO	пув	neu	ьeu	30	Cys	DET	
240	λας	C137	C1 v	_	Dhe	Lev	Δra	Tle		Pro	Δen	Glv	ጥኮዮ		Aen	Glv	
247	ASII	сту	35	птэ	rne	neu	nry	40	Leu	FIU	vah	ОТУ	45	, uı	wah		
248	Thr	Δνα		Δνα	Ser	Acn	Gln		Tle	Gln	Leu	Gln		Ser	Ala	Glu	
250	1 11T	50	vah	лгу	261	чэЬ	55	1113	110	0111	Leu	60	_ ∪u	UCI		J_4	
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251	Ser Val	Glv	Glu	Val	Tvr	Ile	Lvs	Ser	Thr	Glu	Thr	Gly	Gln	Tyr	Leu	
252	65				70					75					80	
253	Ala Met	Asp	Thr		Gly	Leu	Leu	Tyr		Ser	Gln	Thr	Pro		Glu	
254	a1 a		nh -	85	a 1	3	T	~1	90) an	11110	Mirro	Nan	95	mus.	
255 256	Glu Cys	Leu	100		GIU	Arg	Leu	105	GIU	ASII	HIS	TÅL	110	1111	ıyı	
257	Ile Ser	Lvs			Ala	Glu	Lvs		Trp	Phe	Val	Gly		Lys	Lys	
258		115	_			-	120		•			125		-	-	
259	Asn Gly	Ser	Cys	Lys	Arg	Gly	Pro	Arg	Thr	His	Tyr	Gly	Gln	Lys	Ala	
260	130					135	_				140					
261																
262		ייי א איס	TON	EO B		TD NO	. 5			133						
264 (2) INFORMATION FOR SEQ ID NO: 5: 266 (i) SEQUENCE CHARACTERISTICS:																
267 (A) LENGTH: 103 base pairs																
268 (B) TYPE: nucleic acid																
269 (C) STRANDEDNESS: single																
270) TO													
273		SEQ														C 0
275	AGAATTO											JAAC'	ľAG :	TTAAG	TAGTA	60 103
276 278	CGCAAGT								JIAC	.1 G C	AGA					103
280	` '															
280 (i) SEQUENCE CHARACTERISTICS: 281 (A) LENGTH: 103 base pairs																
282 (B) TYPE: nucleic acid																
283		(C) ST	RAND	EDNE	SS: S	sing	le								
284		,) TO													
287		SEQ									aaa			T N N (7)	n a a mma	60
289	TCTGCAG											FACT	AGT :	TAAC:	TAGTTC	60 103
290 292	GATGATI (2) INFO								HIII	JAAI	101					103
294	. ,															
294 (i) SEQUENCE CHARACTERISTICS: 295 (A) LENGTH: 16 base pairs																
296		(B) TY	PE:	nucle	eic a	acid									
297) ST					le								
298		•) TO													
301		SEQ			SCRI	PTIO	N: S	EQ II	O NO	: /:						16
303	GAAATAC				CEO '	או חד	γ. Β									10
307		SEQ														
308	(+)															
309			, TY:													
310) ST					le								
311) TO							-						
314		SEQ			SCRI	PTIO	N: S	EQ I	ON O	: 8:						a =
316	ACTTGGA				CEO :	TD 37	٠. · · ·									17
318	(2) INFO	RMAT SEQ														
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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/902,460

DATE: 12/10/2001 TIME: 11:25:52

Input Set : N:\Crf3\RULE60\09902460.txt Output Set: N:\CRF3\12102001\1902460.raw

L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]